## SEQUENCE LISTING

SEQ ID NO:

Sequenc Length: \40

Sequence Type: Nucleic acid

Strand dn ss: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGAAGTTGC CTGTTAGGCT GTTGGTGCTG

SEQ ID NO: 2

Sequence Length: 39

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGGAGWCAG ACACACTCCT GYTATGGGT

39

SEQ ID NO: 3

Sequence Length: 40

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGAGTGTGC TCACTCAGGT CCTGGSGTTG

SEQ ID NO: 4

Sequence Length: 43

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear -

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGAGGRCCC CTGCTCAGWT TYTTGGMWTC TTG

SEQ ID NO: 5

Sequence Length: 40

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40

43

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Sequence Type: Nucleic acid Strandedn ss: Single Topology: Linear Mol cular Typ : Synth tic DNA Sequence ACTAGTCGAC ATGGATTTWC AGGTGCAGAT TWTCAGCTTC 40 SEQ ID NO: 6 Sequence Length: Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence ACTAGTCGAC ATGAGGTKCY YTGYTSAGYT YCTGRGG 37 SEQ ID NO: 7 Sequence Length: 41 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence ACTAGTCGAC ATGGGCWTCA AGATGGAGTC ACAKWYYCWG G 41 SEQ ID NO: 8 Sequence Length: 41 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence ACTAGTCGAC ATGTGGGGAY CTKTTTYCMM TTTTTCAATT G 41 SEQ ID NO: 9 Sequence Length: 35 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear

<b>\</b>	
Molecular Typ : Synth tic DNA	
Sequence	
ACTAGTCGAC ATGGTRTCCW CASCTCAGTT CCTTG	35
SEQ ID NO: \ 10	
Sequence Length: 37	
Sequence Type: Nucleic acid	
Strandedness: \Single	
Topology: Linear	
Molecular Type: \Synthetic DNA	
Sequence	
ACTAGTCGAC ATGTATATAT GTTTGTTGTC TATTTCT	37
SEQ ID NO: 11	
Sequence Length: 38	
Sequence Type: Nucleic acid	
Strandedness: Single\	
Topology: Linear \	
Molecular Type: Synthetic DNA	
Sequence	
ACTAGTCGAC ATGGAAGCCC CAGCTCAGCT TCTCTTCC	38
SEQ ID NO: 12	
Sequence Length: 27	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA \	
Sequence	
GGATCCCGGG TGGATGGTGG GAAGATG	27
SEQ ID NO: 13	
Sequence Length: 37	
Sequence: Type: Nucleic acid	
Strandedness: Single	
Topology: Linear \	
Molecular Type: Synthetic DNA	
Sequence	
ACTAGTCGAC ATGAAATGCA GCTGGGTCAT STTCTTC	37

SEO ID NO: 14 Sequence Length: 36 Sequence Type: Nucleic acid Strandedness: Singl Topology: Linear Molecular Type: Synthetic DNA Sequence ACTAGTCGAC ATGGGATGGA GCTRTATCAT SYTCTT 36 SEQ ID NO: 15 Sequence Length: 37 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence ACTAGTCGAC ATGAAGWTGT GGTTAAACTG GGTTTTT 37 SEQ ID NO: 16 Sequence Length: 35 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence ACTAGTCGAC ATGRACTTTG GGYTCAGCTT GRTTT 35 SEQ ID NO: 17 Sequence Length: 40 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence -ACTAGTCGAC ATGGACTCCA GGCTCAATTT AGTTTTCCTT 40 SEQ ID NO: 18 Sequence Length: 37 Sequence Type: Nucleic acid

Strandedness: Single			
Topology: Lin ar			
Molecular Type: Synth tic DNA			÷
Sequ nce			
ACTAGTCGAC ATGGCTGTCY TRGSGCTRCT CTTCTGC			37
SEQ ID NO: \ 19	•		
Sequence Length: 36			
Sequence Type: Nucleic acid			
Strandedness: Single			
Topology: Linear			
Molecular Type: Synthetic DNA			
Sequence \			
ACTAGTCGAC ATGGRATGGA GCKGGRTCTT TMTCTT			36
SEQ ID NO: 20			
Sequence Length: \\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\			
Sequence Type: Nucleic acid			
Strandedness: Single			
Topology: Linear \			
Molecular Type: Synthetic DNA			
Sequence \		•	
ACTAGTCGAC ATGAGAGTGC TGATTCTTTT GTG		٠	33
SEQ ID NO: 21			
Sequence Length: 40			
Sequence Type: Nucleic acid			
Strandedness: Single \			
Topology: Linear		,	
Molecular Type: Synthetic DNA			
Sequence			
ACTAGTCGAC ATGGMTTGGG TGTGGAMCTT GCTATTCCTG		·	40
SEQ ID NO: 22 Sequence Length: 37			
Sequence Type: Nucleic acid			
Strandedness: Single			*
Topology: Linear			
Molecular Type: Synthetic DNA			
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Sequ no	
ACTAGTCGAC ATGGGCAGAC TTACATTCTC ATTCCTG	37
SEQ ID NO: 23	
S quence Length: 38	•
Sequence Type: Nucleic acid	
Strandedness: Single	-
Topology: Linear	
Molecular Type: Synthetic DNA	,
Sequence \	
ACTAGTCGAC ATGGATTTTG GGCTGATTTT TTTTATTG	38
SEQ ID NO: 24	
Sequence Length: 37	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	•
Sequence \	
ACTAGTCGAC ATGATGGTGT TAAGTCTTCT GTACCTG	37
SEQ ID NO: 25	
Sequence Length: 28	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
GGATCCCGGG CCAGTGGATA GACAGATG	28
SEQ ID NO: 26	
Sequence Length: 382	
Sequence Type: Nucleic adid	
Strandedness: Double \	
Topology: Linear	
Molecular Type: cDNA	
Original Source	
Organism: Mouse	•
Immediate Source	

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F at	ur	98 :	\ 1.	.72	Sig	j pe	pti	de									
			73.	.38	2 ma	at p	ept	ide								•	
Sequ	en	3															
ATG G	SAG	TCA	CAT	TTA	CAG	GTC	TTT	GTA	TAC	ATG	TTG	CTG	TGG	TTG	TCT		48
Met G	31u	Ser	His	1/12	Gln	Val	Phe	Val	Tyr	Met	Leu	Leu	Trp	Leu	Ser		
				\5					10					15	•		
GGT G	TT	GAT	GGA	GAC	TIA	GTG	ATG	ACC	CAG	TCT	CAA	AAA	TTC	ATG	TCC		96
Gly V					1											`	
			20	_				25				·	30				
					\				•								
ACA T	CA	GTA	GGA	GAC	AGG	GTC	AGC	GTC	ACC	TGC	AAG	CCC	AGT	ÇAG	AAT		144
Thr S	er	Val	Gly	Asp	Arg	₹a1	Ser	Val	Thr	САВ	Lys	Ala	Ser	Gln	Asn		
		35					40					45					
GTG G	GT	ACT	AAT	GTA	GCC	Ted	TAT	CAA	CAG	AAA	CCA	GGG	CAA	TCT	CCT		192
Val G	1y	Thr	Asn	Va1	Ala	Trp	Tyr.	GIn	Gln	Lys	Pro	Gly	Gln	Ser	Pro		
	50					55	\				60						
							\										
AAA C							١.										Z40
Lys P	LO	Leu	Ile	Tyr		Ala	Ser\	Tyr	Arg		Ser	Gly	Val	Pro	-		
65					70			\		75					80		
CGC T	TC	ACA	GGC	ACT	GGA	TOT	GGG	ASA	GAT	<b>ጥፐር</b>	ACT	CTC	ACC	ATC	ACC		288
Arg P								١ ١									
				8.5	,				90					95			
								'	\	•							
AAT G	TG	CAG	TCT	GAA	GAC	TTG	GCA	GAC	TAF	TTC	TGT	CAG	CAA	TAT	AAC		336
Asn V	al	Gln	Ser	Glu	Asp	Leu	Ala	Asp	TXT	Phe	Cys	Gln	Gln	Tyr	Asn		
		,	100					105	\				110				ė
=									\								
AGC T										1					С		382
Ser T	yr	Pro	Arg	ALA	Phe	Gly	Cly	Gly	Thr	As	Leu	Glu	ITe	Lys			

SEQ ID NO: 27

Sequence Length: 409

115

Sequence Type: Nucleic acid

120

125

Strandedness: Double

Topology: Linear

Molecular Type: cDNA Original Sourc Organism: Mouse Immediate Sourc Clone: \pUC-M21-V<sub>II</sub> Features: 1...57 sig peptide 58..409 mat peptide Sequence ATG AAA TGC AGC TGG GTC ATG TTC TTC CTG ATG GCA GTG GTT ACA GGG 48 Met Lys Cys Ser Trp Val Met Phe Phe Leu Met Ala Val Val Thr Gly 10 GTC AAT TCA GAG GTT CAG CTG CAG CAG TCT GGG GCA GAG CTT GTG AAG 96 Val Asn Ser Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys 20 25 CCA GGG GCC TCA GTC AAG TTQ TCC TGC ACA GCT TCT GGC TTC AAC ATT 144 Pro Gly Ala Ser Val Lys Leu\Ser Cys Thr Ala Ser Gly Phe Asn Ile 35 40 AAA GAC ACC TAT ATA CAC TGG GCG AAG CAG AGG CCT GAA CAG GGC CTG 192 Lys Asp Thr Tyr Ils His Trp Ala Lys Gln Arg Pro Glu Gln Gly Leu 50 55 GAG TGG ATT GGA AGG ATT GAT CCT GCG GAT GGT AAT ACT AAA TAT GAC 240 Glu Trp Ile Gly Arg Ile Asp Pro Ala Asp Gly Asn Thr Lys Tyr Asp 75 CCG AAG TTC CAG GGC AAG GCC ACT ATA ACA GCA GAC ACA TCC TCC AAC 288 Pro Lys Phe Gin Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn ACA GCC TAC CTG CAG CTC AGC AGC CTG ACA TCT GAG GAC ACT GCC GTC 336 Thr Ala Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val 100 105 110 TAT TAC TGT GCT TCG GCC TAC TAT GTT AAC CAG GAC TAC TGG GGT CAA 384 Tyr Tyr Cys Ala Ser Ala Tyr Tyr Val Asn Gin App Tyr Trp Gly Gin 115 120

GGA ACC TCA GTC ACC GTC TCC TCA G		409
Gly Thr Ser Val Thr Val Ser Ser		•
130 135		
SEQ ID NO: 28		
Sequence L ngth: 34		
Sequence Type: Nucleic acid		
Strandedness: \Single		
Topology: Linear		
Molecular Type: Synthetic DNA		
Sequence		
GATAAGCTTC CACCATGGGC TTCAAGATGG AGTC		34
SEQ ID NO: 29		
Sequence Length: 34		
Sequence Type: Nucleic acid		
Strandedness: Single \		
Topology: Linear		
Molecular Type: Synthetic DNA		
Sequence	•	
GGCGGATCCA CTCACGTTTG ATTTCCAGTT TGGT		34
SEQ ID NO: 30		
Sequence Length: 43		
Sequence Type: Nucleic acid	•	
Strandedness: Single		
Topology: Linear		
Molecular Type: Synthetic DNA		
Sequence		
GATAAGCTTC CACCATGAAA TGCAGCTGGG TCATGTTCTT CCT		43
SEQ ID NO: 31		
Sequence Length: 34		
Sequence Type: Nucleic acid		
Strandedness: Single		
Topology: Linear		
Molecular Type: Synthetic DNA		
Sequence		
GGCGGATCCA CTCACCTGAG GAGACGGTGA CTGA		34

SEQ ID NO: 32 Sequenc Length: S quence Typ : Nucleic acid Strand dn ss: Single Topology: \Linear Molecular Type: Synthetic DNA Sequence CAGACAGTGG TTCAAAGT 18 SEQ ID NO: 33 Sequence Length 26 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence GAATTCGGAT CCACTCACGT TTGATT 26 SEQ ID NO: 34 Sequence Length: Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence AGTCAGAATG TGGGTACTAA TGTAGCCTGG TACCAGCAGA AGCC 44 SEQ ID NO: 35 Sequence Length: Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence TCCTATCGGT ACAGTGGTGT GCCAAGCAGA TTCAGCGG 38 SEQ ID NO: 36 Sequence Length: Sequence Type: Nucleic acid

Strandedn ss: Singl Topology: Linear Molecular Typ: Synthetic DNA Sequence GCTACCTACT ACTGCCAGCA ATATAACAGC TATCCTCGGG CGTTCGG 47 SEQ ID NO: Sequence Length: Sequence Type:\ Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence ACATTAGTAC CCACATTCTG ACTGGCCTTA CAGGTGATGG TCAC 44 SEQ ID NO: 38 Sequence Length: 47 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence GGCACACCAC TGTACCGATA GGATGCCGAG TAGATCAGCA GCTTTGG 47 SEQ ID NO: 39 Sequence Length: 44 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence GGATAGCTGT TATATTGCTG GCAGTAGTAG QTAGCGATGT CCTC SEQ ID NO: 40 Sequence Length: 379 Sequence Type: Nucleic acid Strandedness: Double Topology: Linear Molecular Type: Synthetic

Original Source	
Organism: Mouse and human	
Immediat \Source	
Clon \ HEF-RVL-M21a-gr	
Amino acid -191:leader	
Amino acid 1 - 23:FR1	
Amino acid 24 - 34:CDR1	
Amino acid 35 - 49:FR2	
Amino acid \ 50 - 56:CDR2	
Amino acid \57 - 88:FR3	
Amino acid 89 - 97:CDR3	
Amino acid 98 - 107:FR4	
Sequence	
ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT	48
Met Gly Trp Ser Cys Ile leu Ser Leu Val Ala Thr Ala Thr Gly	
-19 15 \ -10 -5	
GTC CAC TOC GAC ATC CAG ATG ACC CAG AGC CCA ACC ACC CTG AGC GCC	
Val His Ser Asp Ile GIn Met Thr GIn Ser Pro Ser Ser Leu Ser Ala	96
-1 1 5 10	
AGC GTG GGT GAC AGA GTG ACC ATO ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val	
20 \ 25	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys	
30 35 \ 40	
CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA	2/0
Leu Leu Ile Tyr Ser Als Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	240
45 50 55 60	
TTC AGC GGT AGC GGT AGC GAC TTC AGC TTC AGC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr The Ser Ser	
65 70 \ 75	

CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC 336 Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser 80 TAT CCT CGG CCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C 379 Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 95 100 105 SEQ ID NO: Sequence Length: 31 Sequence Type: \ Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence GGTACCGACT ACACCTTCAC CATCAGCAGC C 31 SEQ ID NO: 42 Sequence Length: 31 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence GGTGAAGGTG TAGTCGGTAC CGCTACCGCT A 31 SEQ ID NO: 43 Sequence Length: 379 Sequence Type: Nucleic acid Strandedness: Double Topology: Linear: Molecular Type: Synthetic Original Source Organism: Mouse and human Immediate Source Clone: HEF-RVL-M21b-gk Amino acid -19--1:leader Amino acid 1 - 23:FR1 Amino acid 24 - 34:CDR1

35 - 49:FR2

Amino acid

	A	mįn	o ac	id	. 50	- 5	6:C	DR2									
	A	min	e ac	id	57	- 8	38:F	R3									
	A	min	o ac	id	89	- 9	7:C	DR3									
٠	A	mine	o ac	<b>4</b> d	98	- ]	107:	FR4									
Seg	uen	Ce															
ATG	GGA	TGG	AGC	TGT	ATC	ATC	CTC	TCC	TTG	GTA	GCA	ACA	GCT	ACA	GGT		48
					<b>\</b>		Leu										
-19				-15					-10					-5			
					,												
						\	ACC										96
Val	His			Ile	Gln	Me£	Thr	Gln	Ser	Pro	Ser	Ser		\$er	Ala		
		-1	1					3					10				
AGC	GTG	GGT	GAC	AGA	GTG	ACC	ATE	ACC	TGT	AAG	GCC	AGT	CAG	AAT	GTG		144
							Ile										
		15					20			-		25					
							ÇAG		`							٠.	192
Gly		Asn	Val	Ala	Trp		Gln	Gln	LXs	Pro		Lys	Ala	Pro	Lys	•	
	30					35			\	\	40						
CTG	CTG	ATC	TAC	TCG	GCA	TCC	TAT	rec	TAC	AGT	GCT.	GTG	CCA.	AGC	AGA		240
							Tyr			<b>\</b>							240
45					50		-,-		-,-	55	/				60		
TTC	AGC	GGT	AGC	GGT	AGT	GGT	ACC	GAC	TAC	ACC	TTC	ACC	ATC	AGC	AGC		288
Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Tyr	Thr	Phe	khr	Ile	Ser	Ser		
				65					70					75			
CTC	CAG	CCA	CAC	CAC	A T.C	ccc	100	TAC	T.A.C.	WCC	CAC		<b>A</b>	446	400		224
Leu									-				•			-	336
			80					85	- , -	<b>-</b> , -	• • • • • • • • • • • • • • • • • • • •	<b>J</b> 2	90	/	061		
													•				
TAT	CCT	CGG	GCG	TTC	GGC	CAA	GGG	ACC	AAG	GTG	GAA	ATC	AAA	c \	\		379
Tyr	Pro		Ala	Phe	Gly	Gln	Gly	Thr	Lys	Val	G1u	I1e	Lys				
		95					100					105					
SEQ				_											'		
Seq			_		29												
Seq	ueno	Ce T	Abe	= 1	luc l	eic	aci	Ld		٠							

Strandedness: Singl Topology: Linear Mol cular Type: Synth tic DNA Sequence GCTACCTACT TCTGCCAGCA ATATAACAG 29 SEQ ID NO: Sequence Length: 29 Sequence Type: \ Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence TGCTGGCAGA AGTAGGTAGC GATGTCCTC 29 SEQ ID NO: 46 Sequence Length: 379 Sequence Type: Nucleid acid Strandedness: Double Topology: Linear Molecular Type: Synthetic Original Source Organism: Mouse and human Immediate Source Clone: HEF-RVL-M21c-gk Amino acid -19--1:leader Amino acid 1 - 23:FR1 Amino acid 24 - 34:CDR1 Amino acid 35 - 49:FR2 Amino acid 50 - 56:CDR2 Amino acid 57 - 88:FR3 Amino acid 89 - 97:CDR3 Amino acid 98 - 107:FR4 Sequence ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala The Ala Thr Gly -19 -15 -10

Amino acid

1 - 23:FR1

GTC	CAG	TCC	GAC	ATC	CAG	ATG	ACC	CAG	AGC	CCA	AGC	AGC	CTG	AGC	GCC		96
Val	His	Ser	Asp	Il	Gln	Met	Thr	G1n	Ser	Pro	Ser	Ser	Leu	Ser	Ala		
		71	. 1					5					10				
AGC	GTG	GGT	GAC.	AGA	GTG	ACC	ATC	ACC	TGT	AAG	GCC	AGT	CAG	AAT	GTG		144
Ser	Val	Gly	Asp	Arg	Va1	The	I1e	Thr	Сув	Lys	Ala	Ser	Gln	Asn	Val		
		15	\				20					25					
GGT	ACT	AAT	GTA	cdc	TGG	TAC	CAG	CAG	AAG	CCA	GGA	AAG	GCT	CCA	AAG		192
Gly	Thr	Asn	Val	Alà	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys		•
	30			`	\	35					40						
						_											
CTG					١												240
Leu 45	reu	ITS	175	ber	50\	ser	Tyr	Arg	Tyr	Ser 55	GIA	Val	Pro	Ser	_		
• • •	•		•		201	(				<b>د</b> د					60		
TTC	AGC	GGT	AGC	GGT	AGC	GGT	ACC	GAC	TTC	ACC	TTC	ACC	ATC	AGC	AGC		288
Phe						١ ١											
				65		\	\	_	70					75			
CTC							\										336
Leu	Gln	Pro		Asp	Ile	Ala	Thr		Phe	Cys	G1n	Gln		Asn	Ser		
			80					85					90				
TAT	CCT	CGG	GCG	TTC	GGC	CAA	GGG	ACE	AAG	GTG	GAA	ATC	AAA	c			379
Tyr								\						_			•
		95			•		100	,	\			105	•				
SEQ	ID	NO:	4	7											÷		
Şequ	enc	e L	eng	thi	37	9			\							• •	
Sequ	enc	:e T	ype	: 1	Nucl	eic	ac:	id	,	\							
Stra	ande	edne	881	Do	oub1	<b>.e</b>											
Topo	olog	IY:	Li	neaz	<b>C</b> .					\							
Mole					Syn	the	tic			'	\						
Orig	jine	ıl S	our	C 😝 :													
	Oz	gan	ism	: M	lous	e a	nd l	ıuma	n		\						
Imme	edia	ite	Sou	rce							'	\					
	CI	one	: ]	HEF-	RVL	-M2	ld-ç	ξK									
				id -			_		•			\					
												\					

Amino acid	24 - 34:CDR	1	
Amino acid	.35 - 49:FR2		
Amino acid	50 - 56:CDR	2	
Amino \acid	57 - 88:FR3		
Amino acid	.89 - 97:CDR	3 .	
Amino acid	98 - 107:FR	4	
Sequence			•
ATG GGA TGG AGC TGT	ATC ATC CTC TO	C TTG GTA GCA ACA GC1	ACA GGT 48
	: Île Ile Leu Se	r Leu Val Ala Thr Ala	Thr Gly
-19 -15	, /	-10	-3
GTC CAC TCC GAC ATC	CAG ATG ACC CA	G AGC CCA AGC AGC CTG	AGC GCC 96
	\	n Ser Pro Ser Ser Leu	
-1 1	1	5 10	
	\		
	\	C TGT AAG GCC AGT CAG	
Ser var Gly Asp Arg	var int iffe in	r Cys Lys Ala Ser Gln 25	ASU AST
20	-7		
GGT ACT AAT GTA GCC	TGG TAC CAG CA	G AAG CCA GGA AAG GCT	CCA AAG 192
	Trp Tyr Gin G	n Lys Pro Gly Lys Als	Pro Lys
30	35	<b>\</b> 40	
CTG CTG ATC TAC TCG	GCA TCC TAT CG	G TAC AGT GGT GTG CCA	AGC AGA 240
		Tyr Ser Gly Val Pro	
45	50	55	60
		TAC ACC TTC ACC ATC	
of the ser Gly ser Gly	Ser Gly Inr As	o fyr Thr Phe Thr 11e	ser ser 75
. 03		,,	73
CTC CAG CCA GAG GAC	ATC GCC ACC TA	TTC TGC CAG CAA TAT	AAC AGC 336
	Ile Ala Thr Ty	Phe Cys Gln Gln Tyr	Asn Ser
80	8:	90	,
TAT CCT CGG GCG TTC	GGC CAA GGG AC	AAG GTG GAA ATC\AAA	C 379
		Lys Val Glu Ile Ays	
95	100	105	
SEQ ID NO: 48			
Sequence Length:	29		

Sequence

S quenc Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence TGACAGAGTG\TCCGTCACCT GTAAGGCCA SEQ ID NO: Sequence Length: Sequence Type:\ Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence TTACAGGTGA CGGACACTOT GTCACCCAC SEQ ID NO: 50 Sequence Length: 379 Sequence Type: Nucleid acid Strandedness: Double Topology: Linear Molecular Type: Synthetia Original Source Organism: Mouse and human Immediate Source Clone: HEF-RVL-M21e-gk Amino acid -19--1:leader 1 - 23:FR1 Amino acid Amino acid 24 - 34:CDR1 Amino acid 35 - 49:FR2 Amino acid. 50 - 56:CDR2 Amino acid 57 - 88:FR3 Amino acid 89 - 97:CDR3 Amino acid 98 - 107:FR4

29

ATG	GEA	TGG	AGC	TGT	ATC	ATC	CTC	TCC	TTG	GTA	GÇA	ACA	GCT	ACA	GGT		48
Met	CI3	Trp	Ser	Cys	Ile	Ile	Leu	Ser	Leu	Val	Ala	Thr	Ala	Thr	Gly		
-19				-15					-10					-5			
GTC	CAC	TCC	GAC	ATC	CAG	ATG	ACC	CAG	AGC	CCA	AGC	AGC	CTG	AGC	900		96
		Ser	\														
			7,1					5					10				
			\	\													
		GGT		\													144
Ser	Val	Gly	Asp	VLE	VAI	Ser		Thr	Cys	Lys	Ala		Gln	Asn	Val		
		15					20					25					
GGT	ACT	AAT	GTA	GCC	TCE	TAC	CAG	CAG	AAG	CCA	GGA	AAG	GCT	CCA	AAG		192
Gly	Thr	Asn	Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	A1a	Pro	Lys		
	30					\35					40					•	
CŤC	C TrC	A TC	TAC	<b>T</b> CC	CC 4	TCA	77 A 77	CCC	m. c	A 77 <b>77</b>		C.T.C		400	464		
		ATC Ile				,	١.										240
45	204		•,•	501	50	261	۲,۰		*,-	55.	or,	7 64 4		OCL	60		
							- 1										
TTC	AGC	GGT	AGC	GGT	AGC	GGT	vcc/	GAC	TTC	ACC	TTC	ACC	ATC	AGC	AGC		288
Phe	Ser	Gly	Ser	Gly	Ser	G1 <b>y</b>	Thr	yab	Phe	Thr	Phe	Thr	Ile	Ser	Ser		
				65			•		70					75			
CTC	CAG	CCA	GAG	GAC	ATC	GCC	ACC	TAC	TAC	TGC	CAG	CAA	ፐልጥ	AAC	AGC		336
Leu								,	\								<i>-</i>
			80	-				85	/				90				
								•									
TAT										1				С		-	379
Tyr	Pro	Arg 95	VÍT	Phe	Gly	GIn	Gly 100	Thr	Lys	API	Glu		Lys			•	
SEQ	TD		5	1			100					105					
Sequ					37	· q.				\	\						
Sequ			_		-		AC S	d									
Stra											\						
Topo						. 🕶					1	\					
Mole	-					the	ti~										
Orig					~ X 11							\					
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Imme		-			10.11Q	a a	iu I	. Willid	41								
uite	-416		JJu.										- /				

Clone: HEF-RVL-M21f-gr	
Amino acid -191:leader	
Amino acid 1 - 23:FR1	
Amino acid 24 - 34:CDR1	
Amino acid 35 - 49:FR2	
Amino acid 50 - 56:CDR2	
Amino acid \57 - 88:FR3	
Amino acid 89 - 97:CDR3	
Amino acid 98 - 107:FR4	
Sequence	
ATG GGA TGG AGC TGT ATC ATG CTC TCC TTG GTA GCA ACA GCT ACA GC	GT .48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr G	
-19 -15 \ -10 -5	
	•
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC CTG AGC GC	
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Al	
\	
AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GT	G 144
Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Va	· <b>1</b>
20 \ 25	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AA	_
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Ly	
30 35 40	8
CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GCT GTG CCA AGC AG	
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Ar	g
45 50 55 6	0
TTC AGC GGT AGC GGT ACC GAC TTC ACC ATC AGC AGC	700
Phe Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Se	
65 70 75	
	•
CTC CAG CCA GAG GAC ATC GCC ACC TAC TTC TGC CAG CAA TAT AAC AGC	
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Sei	•
85 90	

TAT OCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C 379 Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 100 SEQ ID NO: 52 Sequence Length: 26 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence GACTTCACCT TGACCATCAG CAGCCT 26 SEQ ID NO: 53 Sequence Length: \26 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence CTGCTGATGG TCAAGGTGAA GTCGGT 26 SEQ ID NO: 54 Sequence Length: Sequence Type: Nucleic acid Strandedness: Double Topology: Linear Molecular Type: Synthetic Original Source Organism: Mouse and human Immediate Source Clone: HEF-RVL-M21g-gk Amino acid -19--1:leader Amino acid 1 - 23:FR1 Amino acid 24 - 34:CDR1 Amino acid 35 - 49:FR2 Amino acid 50 - 56:CDR2 Amino acid 57 - 88:FR3

Amino acid 89 - 97:CDR3 '
Amino acid 98 - 107:FR4

Molecular Type: Synthetic

Socuence	
Sequence	4.5
ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT	•
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	•
-19 \-15 \-10 \-5	•
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
-1 1 \ 5 \ \	
AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val	
15 20 25	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gin Gln Lys Pro Gly Lys Ala Pro Lys	
30 35 40	
CTG CTG ATC TAC TCG GCA TCC TAT GGG TAC AGT GGT GTG CCA AGC AGA	240
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	
45 50 \ 55 60	
TTC AGC GGT AGC GGT AGC GAC TTC ACC TTG ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser	
65 70 75	
CTC CAG CCA GAG GAC ATC GCC ACC TAC TTC TGC CAG CAA TAT AAC AGC	
Leu Gin Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gin Gin Tyr Asn Ser	
80 85 \ 90	
TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C	379
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	
95 100 \ 105	
SEQ ID NO: 55	
Sequence Length: 379	
Sequence Type: Nucleic acid	
Strandedness: Double	
Topology: Linear	

Original Sourc	
Organism: Mouse and human	
Immediate Sourc	
Clon: HEF-RVL-M21h-gx	
Amino acid -191:leader	
Amino acid 1 - 23:FR1	
Amino acid 24 - 34:CDR1	
Amino acid 35 - 49:FR2	
Amino acid 50 - 56:CDR2	•
Amino acid 57 - 88:FR3	
Amino acid 89 - 97:CDR3	
Amino acid 98 - 107:FR4	
Sequence	
ATG GGA TGG AGG TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT	. 48
Met Gly Trp Ser Cys 11e Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	
-19 -15 -10 -5	
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
-1 1 5 10	
AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val	,
15 20 25	•
	•
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys 30 35 40	•
	•
CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA	240
Lau Lau Ila Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	
45 50 55 60	
TTC AGC GGT AGC GGT AGC GAC TTC ACC TTG ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser	<del>-</del> _
65 70 75	•

CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC	336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser	
80 85 90	
TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C	379
Tyr Pro Arg Ala Phe Gly Gin Gly Thr Lys Vai Glu Ile Lys	
95 100 105	
SEQ ID NO: 56	
Sequence Length: 29	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
GGACAGAGTC CAAAGCCGCT GATCTACTC	29
SEQ ID NO: 57	
Sequence Length: 29	
Sequence Type: Nucleic acid	
Strandedness: Single	,
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
ATCAGCGGCT TTGGACTCTG TCCTGGCTT	29
SEQ ID NO: 58	
Sequence Length: 379	
Sequence Type: Nucleic acid	
Strandedness: Double	
Topology: Linear	
Molecular Type: Synthetic	
Original Source	
Organism: Mouse and human	
Immediate Source	
Clone: HEF-RVL-M21i-g*	
Amino acid -191:leader	
Amino acid 1 - 23:FR1	
Amino acid 24 - 34:CDR1	

Amino acid 35 - 49:FR2 Amino acid . 50 - 56:CDR2 Amino acid 57 - 88:FR3 Amino acid 89 - 97:CDR3 Amino acid 98 - 107:FR4 Sequence ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT 48 Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly -19 -15 -10 - 5 GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC 96 Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG 144 Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val 15 20 25 GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG 192 Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys 30 35 40 CCG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA 240 Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg 45 50 TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTG ACC ATC AGC AGC 288 Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser 65 70 75 CTC CAG CCA GAG GAC ATC GCC ACC TAC TTC TGC CAG CAA TAT AAC AGC 336 Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser 80 90 TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C 379 Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 95 100 105 SEQ ID NO: 59 Sequence Length: 26 Sequence Type: Nucleic acid

Strand dness: Singl Topology: Lin ar Molecular Type: Synthetic DNA Sequence GAGGACATCG CTGACTACTT CTGCCA 26 SEQ ID NO: 60 Sequence Length: 26 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence 26 AAGTAGTCAG CGATGTCCTC TGGCTG SEQ ID NO: 61 Sequence Length: 379 Sequence Type: Nucleic acid Strandedness: Double Topology: Linear Molecular Type: Synthetic Original Source Organism: Mouse and human Immediate Source Clone: HEF-RVL-M21j-gk Amino acid -19--1:leader Amino acid 1 - 23:FR1 Amino acid 24 - 34:CDR1 Amino acid 35 - 49:FR2 Amino acid 50 - 56:CDR2 Amino acid 57 - 88:FR3 Amino acid 89 - 97:CDR3 Amino acid 98 - 107:FR4 Sequence ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT 48 Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly -5 -19 -15 -10

GTC	CAC	TCC	GAC	ATC	CAG	ATG	ACC	CAG	AGC	ССА	AGC	AGC	CTG	AGC	GCC		96
		Ser															90
		- 1	•		-			5					10				
										•							
		GGT															144
Ser	Val	Gly	Aep	Arg	Val	Ser		Thr	Cys	Lys	Ala		GIn	Asn	Val		
		15					20					25					
GGT	ACT	AAT	GTA	GCC	ŤGG	TAC	CAG	CAG	AAG	CCA	GGA	CAG	AGT	CCA	AAG		192
		Asn															
	30				_	35				•	40				·		
		ATC									-	-					240
Pro 45	Leu	Ile	Tyr	Ser	A1a 50	Ser	Tyr	Arg	Tyt		Gly	Val	Pro	Ser	-		
• •					20					55					60		•
TĨG	AGC	GGT	AGC	GGT	AGC	GGT	ACC	GAC	TTC	ACC	TTG	ACC	ATC	AGC	AGC		288
Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser		
				65					70					75			
		CCA														-	336
Leu	GIN	Pro	80	vab	116	VIE	Asp	1 y r 8 5	rne	Cy 5	GIN	GIR	90	Asn	Ser		
			•					03					34		•		
TAT	CCT	CGG	GCG	TTC	GGC	CAA	GGG	ACC	AAG	GTG	GAA	ATC	AAA	С			379
Tyr	Pro	Arg	Ala	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	11e	Lys				
		95		_			100			•		105					
_		NO:		_													
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Seq							aci	ld									
Str	ande	edne	851	Do	publ									•			
Topo	•			neaı	•												
Mol	ecu]	lar	Тур	<b>e</b> 1	Syn	the	tic										
Ori	gina	al S	our	C <del>0</del>													
	01	rgan	ism	<b>:</b> }	lous	e a	nd t	านฑล	n		•						
Imme	edia	ate	Sou	rce													
	CI	lone	: 1	HEF-	RVL	-M2	lk-ç	jκ									·

Amino acid -19--1:leader

Amino acid

1 - 23:FR1

Amino acid 24 - 34:CDR1

	A	mino	ac	id	. 35	- 4	9:F	R2								
	Ai	mino	ac	id	50	- 5	6 : C	DR2								
	Aı	mino	ac	id	57	- 8	8:F	R3								
		_					7 : C									
							07:									
Segi			, ac	TU	20	- 1	.071	r W.A.								
ATG			AGC	ተርተ	ATC	ATC	СТС	TCC	TTG	GTA	GCA	ACA	GCT	ACA	GGT	48
Met																
-19	,			-15		<b>4</b>			-10					-5	•	
GTC	CAC	TCC	GAC	ATC	CAG	ATG	ACC	CAG	AGC	CCA	AGC	AGC	CTG	AGC	GCC	96
Val	His	Ser	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	
		-1	1					5					10			
															686	4.4
															GTG	. 144
Ser	VAI	15	wab	Arg	VAI	Ser	20	1112	Сув	Lys	UTS	25	GIII	Vali	***	
		13					20									
GGT .	ACT	AAT	GTA	GCC	TGG	TAC	CAG	CAG	AAG	CCA	GGA	AAG	GCT	CCA	AAG	192
Gly																
-	30				_	35					40					
			•													
CTG																240
Leu	Leu	Ile	Tyr	Ser		Ser	Tyr	Arg	Tyr		Gly	Val	Pro	Ser		
45					50					55					60	
TTC .	ACC	CCT	ACC	GGT	AGC	COT	ACC	GAC	TTC	ACC	TTG	ACC	ATC	AGC	AGC	288
Phe																200
		01,		65		01)			70					75		
CTC	CAG	CCA	GAG	GAC	ATC	GCC	GAC	TAC	TTC	TGC	CAG	CAA	TAT	AAC	AGC	336
Leu	G1n	Pro	Glu	Asp	lle	Ala	Asp	Tyr	Phe	Cys	Gln	Gln	Tyr	Asn	Ser	
			80					85					90			
														_		270
TAT														U		379
Tyr	110	Arg 95	WIS	rne	GIA	ATE	100	int	r) a	441	GIU	105	-ya			
SEQ	חד			3												
_					2.	, a										
Sequence Length: 379																

Sequenc Type: Nucleic acid

Strandedness: Doubl Topology: Linear Molecular Type: Synthetic Original Source Organism: Mouse and human Immediate Source Clone: HEF-RVL-M211-gk Amino acid -19--1:leader Amino acid 1 - 23:FR1 Amino acid 24 - 34:CDR1 Amino acid 35 - 49:FR2 Amino acid 50 - 56:CDR2 Amino acid 57 - 88:FR3 Amino acid 89 - 97:CDR3 Amino acid 98 - 107:FR4 Sequence ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT 48 Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly -19 -15 GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC 96 Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala -1 1 AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG 144 Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val 15 20 GGT ACT AAT GTA CCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG 192 Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys 30 35 CCG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA 240 Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg 45 50 55

Immediate Source

TTC AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser	
65 70 75	-
CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC	336
Leu Gin Pro Giu Asp fle Ala Thr Tyr Tyr Cys Gin Gin Tyr Asn Ser	
80 85 90	
	379
TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	3/9
95 100 105	
SEQ ID NO: 64	
Sequence Length: 26	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
CAGAGCCAAA AGTTCCTGAG CGCCAG	26
SEQ ID NO: 65	
Sequence Length: 26	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
CTCAGGAACT TTTGGCTCTG GGTCAT	26
SEQ ID NO: 66	
Sequence Length: 379	
Sequence Type: Nucleic acid	
Strandedness: Double	
Topology: Linear	
Molecular Type: Synthetic	
Original Source	
Organism: Mouse and human	

Clone: HEF-RVL-M21m-gx														
Amino acid -191:lead r														
Amino cid 1 - 23:FR1														
Amino acid 24 - 34:CDR1														
Amino acid 35 - 49:FR2														
Amino acid 50 - 56:CDR2														
Amino acid 57 - 88:FR3														
Amino acid 89 - 97:CDR3														
Amino acid 98 - 107:FR4														
Sequence														
ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT	48													
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly														
-19 -15 -10 -5	-													
·	2.5													
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CAA AAG TTC CTG AGC GCC	96													
Val His Ser Asp Ile Gln Met Thr Gln Ser Gln Lys Phe Leu Ser Ala -1 1 5 10														
AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG	144													
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val														
15 20 25														
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG	192													
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys														
30 . 35 40														
CCG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA	240													
Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg 45 50 55 60														
45 50 55 60														
TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC	288													
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser														
<b>65</b>														
	400													
CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC	336													
Leu Gin Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gin Gin Tyr Asn Ser 80 85 90														
,														

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	379
95 100 105	
SEQ ID NO: 67	
Sequence Length: 29	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
GGACAGAGTC CAAAGCTGCT GATCTACTC	29
SEQ ID NO: 68	
Sequence Length: 29	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	,
Molecular Type: Synthetic DNA	
Sequence	
ATCAGCAGCTT TGGACTCTG TCCTGGCTT	29
SEQ ID NO: 69	
Sequence Length: 379	
Sequence Type: Nucleic acid	
Strandedness: Double	
Topology: Linear	
Molecular Type: Synthetic	
Original Source	
Organism: Mouse and human	
Immediate Source	
Clone: HEF-RVL-M21n-gk	
Amino acid -191:leader	
Amino acid 1 - 23:FR1	
Amino acid 24 + 34:CDR1	
Amino acid 35 - 49:FR2	
Amino acid 50 - 56:CDR2	
Amino acid 57 - 88:FR3	

Amino	acid	89	-	97:CDR3
Amino	acid	98	_	107:FR4

Segu	nce
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ATG GGA TGG	AGC TGT ATC	ATC CTC TCC	TTG GTA GCA ACA	GCT ACA GGT	48
Met Gly Trp	Ser Cys Il	Ile Leu Ser	L u Val Ala Thr	Ala Thr Gly	
-19	-15	*	-10	-5	

GTC CAC TCC G	AC ATC CAG	ATG ACC CAG AG	C CCA AGC AGC CTG	AGC GCC 96
Val His Ser A	sp Ile Gln	Met Thr Gln Se	r Pro Ser Ser Leu	Ser Ala
_1	1	•	10	

AGC	GTG	GGT	GAC	AGA	GTG	ACC	ATC	ACC	TGT	AAG	GCC	AGT	CAG	AAT	GTG	144
Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Lys	A1a	Ser	Gln	Asn	Val	
		4.6					20					78				

GGT ACT AAT	GTA GCC TGG TAC CAG CAG	AAG CCA GGA CAG AGT	CCA AAG 192
Gly Thr Asn	Val Ala Trp Tyr Gln Gln	Lys Pro Gly Gln Ser 1	Pro Lys
30	35	40	

CTG C	TG	ATC	TAC	TCG	GCA	TCC	TAT	CGG	TAC	AGT	GGT	GTG	CCA	AGC	AGA	240
Leu Le	eu	I1e	Tyr	Ser	Ala	Ser	Tyr	Arg	Tyr	Ser	Gly	Val	Pro	Ser	Arg	
45					50					55					60	

TTC	AGC	GGT	AGC	GGT	AGC	GGT	ACC	GAC	TTC	ACC	TTC	ACC	ATC	AGC	AGC	288
Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Phe	Thr	Ile	Ser	Ser	
				65					70					75		

CTC	CAG	CCA	GAG	GAC	ATC	GCC	ACC	TAC	TAC	TGC	CAG	ÇAA	TAT	AAC	AGC	336
Leu	Gln	Pro	Glu	Asp	Ile	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Tyr	Asn	Ser	
			80					85					90			

TAT CCT CGG GCG	TTC GGC CAA GGG	ACC AAG GTG GAA	ATC AAA C 3	79
Tyr Pro Arg Ala	Phe Gly Gin Gly	Thr Lys Val Glu	Ile Lys	
95	100	)	105	

SEQ ID NO: 70

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

									- 7	7 -						
Ori	gin	al S	Sour	C			•									
	0	rgai	nism	l <b>:</b>	Mous	se 8	ind	huma	n							
Imm	edi	ate	Sou	rce												
	С	lone	e:	HEF	-RVI	L-M2	?1o-	gr								
	A	mino	o ac	id	-19-	1:	lea	der			÷	•				
	A	mino	o ac	id	1	- 2	3 : F	R1								
					24											
					35											
	_	•			50											
					57											
					_											
					89											
			o ac	id	98	- ]	07:	FR4								
-	nen															
								TCC								48
-19	GIY	Trp	Ser	-15		116	Leu	Ser	-10	ANT	Ala	inr	VIE	-5	Gly	
-72				-13			•		-10					- 3		
GTC	CAC	TCC	GAC	ATC	CAG	ATG	ACC	CAG	AGC	CCA	AGC	AGC	CTG	AGC	GCC	96
Va1	His	Ser	Asp	Ile	Gln	Met	Thr	G1n	Ser	Pro	\$er	Ser	Leu	Ser	Ala	
		-1	1					5					10			
								ACC								144
ser	VAI	G1 <b>y</b>	Asp	Arg	VBI	The	20	Thr	Cys	Lys	Ala	25	GIN	AWN	VAI	
		13					20	*				دے				
GGT	ACT	AAT	GTA	CCC	TGG	TAC	CAG	CAG	AAG	CCA	GGA	CAG	AGT	CCA	AAG	192
								Gln								
	30					35				•	40					•

CCG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg

TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser

CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC	336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser	
80 85 90	
TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C	379
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	3,7
35 100 105	
SEQ ID NO: 71	
Sequence Length: 23	
Sequence Type: Nucleic acid	• • •
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
GCTCCAAAGC CGCTGATCTA CTC	23
SEQ ID NO: 72	
Sequence Length: 23	
Sequence Type: Nucleic acid	-
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
TAGATCAGCG GCTTTGGAGC CTT	23
SEQ ID NO: 73	
Sequence Length: 379	
Sequence Type: Nucleic acid	
Strandedness: Double	
Topology: Linear	
Molecular Type: Synthetic	
Original Source	
Organism: Mouse and human	
Immediate Source	
Clone: HEF-RVL-M2lp-gk	
Amino acid -191:leader	
Amino acid 1 - 23:FR1	
Amino acid 24 - 34:CDR1	

	۸ı	mine	, ac	id	25	_ 4	O . F	R2								
				id												
	-															
				id												
				id							*					
	Aı	mino	ac	id	98	- 1	.07:	FR4								
Seq	uen	C e														
				TGT												48
Met	Gly	Trp	Ser	Cys	Ile	I1e	Leu	Ser		Va1	Ala	Thr	Ala		Gly	
-19				-15					-10					- 5		
	C.A.C.	TÓD	CAC	ATC	CAC	A TC	A C C	CAC	۸۵۵	CCA	AGC.	AGC	CTG	AGC	acc	96
				Ile												30
***	11.7.9	-1	73 P	116	JIII	rie c	****	5	UEI		•••	***	10	-		
			•					_								
AGC	GTG	GGT	GAC	AGA	GTG	ACC	ATC	ACC	TGT	AAG	GCC	AGT	CAG	AAT	GTG	144
Ser	Val	Gly	Asp	Arg	Va1	Thr	île	Thr	Суз	Lys	Ala	Ser	Gln	Asn	Va1	
		15					20					25				
										•					AAG	192
Gly		Asn	Va1	Ala	Trp	-		Gin	Lys	Pro		Lys	Ala	Pro	Lys	•
	30					35		•			40					
			m.c	TCC		TOC	~~			ACT	CCT	CTC	CCA	<b>ACC</b>	AGA	240
				Ser												240
45	Deu	116	ıyı	ser	50	Ser	171	VrR	171	55	Gly	Val	110	041	60	
7.5					-					•••						
TTC	AGC	GGT	AGC	GGT	AGC	GGT	ACC	GAC	TTC	ACC	TTC	ACC	ATC	AGC	AGC	288
Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Phe	Thr	Ile	Ser	Ser	
				65					70					75		
								•								
				GAC												336
Leu	Gln	Pro		Asp	Ile	Ala	Thr		Tyr	Cys	Gln	Gln		Asn	Ser	
			80					85					90			
тат	CCT	ccc.	CCC.	TTC	GGC	CAA	ccc	ACC	AAG	GTG	GAA	ATC	AAA	<b>c</b> .		379
				Phe												2
.,-		95			,		100		- <b>,</b> -			105				
SEO	ID	NQ:	. 7	4												
		ce I			13	37										
_			_		i. Nucl			: A	•							٠
aad	741I	ce 1	. y pa	•	MUC I	r <del>a</del> YC	ac.	-4								

AGGATCAATC CT

Strandedness: Singl Topology: Linear Molecular Type: Synth tic DNA S qu nc AAGAAGCCTG GGTCCTCAGT GAAGGTCTCC TGCAAGGCTT CTGGCTTCAA CATTAAAGAC 60 ACCTATATAC ACTGGCTGCG CCAGGCTCCA GGACAGGGCC TGGAGTGGAT GGGAAGGATT 120 137 GATCCTGAGG ATGGTAA SEQ ID NO: 75 Sequence Length: 111 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence TGAGATCTGA GGACACAGCC TTTTATTTCT GTGCAAGTGC CTACTATGTT AACCAGGACT 60 ACTGGGGCCA AGGGACCACT GTCACCGTCT CCTCAGGTGA GTGGATCCGA C 111 SEQ ID NO: 76 Sequence Length: 130 Sequence Type: Nucleic acid Strandedness: Single Topology: Linear Molecular Type: Synthetic DNA Sequence ACCTTCACTG AGGACCCAGG CTTCTTCACC TCAGCTCCAG ACTGCACCAG CTGCACCTGG 60 GAGTGAGCAC CTGGAGCTAC AGCCAGCAAG AAGAAGACCC TCCAGGTCCA GTCCATGGTC 120 GAAGCTTATC 130 SEQ ID NO: 77 Sequence Length: 132 Sequence Type: Nucleic acid Strandedness: Single: Topology: Linear Molecular Type: Synthetic DNA Sequence AAAGGCTGTG TCCTCAGATC TCAGGCTGCT GAGCTCCATG TAGGCTGTGT TCGTGGATTC 60 GTCTGCAGTG ATTGTGACTC GGCCCTGGAA CTTCGGGTCA TATTTAGTAT TACCATCCGC 120

SEQ ID NO: 78 Sequence L ngth: 25 S quence Type: Nucl ic acid Strandedness: Single Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GATAAGCTTC CACCATGGAC TGGAC

SEQ ID NO: 79

Sequence Length:

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GTCGGATCCA CTCACCTGAG GAGAC

SEQ ID NO: 80

Sequence Length: 409

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVH-M21-gyl

Amino acid -19--1:leader

Amino acid 1 - 30:FR1

Amino acid 31 - 35:CDR1

Amino acid 36 - 49:FR2

Amino acid 50 - 66:CDR2

Amino acid: 67 - 98:FR3

Amino acid 99 - 106:CDR3

Amino acid 107 - 117:FR4

Sequence

25

ATG	GAC	TGG	ACC	TGG	AGG	GTC	TTC	TTC	TTG	CTG	GCT	GTA	GCT	CCA	GGT	48
Met	Asp	Trp	Thr	Trp	Arg	Va1	Phe	Phe	Leu	Leu	Ala	Val	Ala	Pro	G1y	
-19				-15					-10					-5		
GCT	CAC	TCC	CAG	GTG	CAG	CTG	GTG	CAG	TCT	GGA	GCT	GAG	GTG	AAG	AAG	96
Ala	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	G1y	Ala	Glu	Val	Lys	Lys	
		-1	1					5					10			
,																
					AAG											. 144
Pro	Gly	Ser	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Phe	Asn	Ile	
		15					20					25				8
					CAC											192
Lys		Thr	Tyr	Ile	His	_	Val	Arg	Gln	Ala		Gly	Gln	Gly	Leu	
	30					35					40					
GAG						-										240
GIu	Trp	Met	Gly	Arg		Asp	Pro	Ala	Asp		Asn	Thr	Lys	Tyr		
45					50					55					50	
CCG	A A C	TTC	CAC	ccc	CCA	CTC	A C A	4 TC	ACT	CC'A	CAC	CAA	T.C.C	ACC	440	288
Pro																200
710	⊥y s	FILE	GIII	65	vr R	V#1	IIIL	116	70	WIG	voh	<b>GI</b> I	DEL	75	Volt	
				<b>V</b>					, ,					,,		
ACA	GCC	TAC	ATG	GAG	СТС	AGC	AGC	CTG	AGA	тст	GAG	GAC	ACA	GCC	<b>ፓ</b> ተ <b>ዮ</b>	336
															Phe	
		-,-	80					85					90			
			••					••								-
TAT	TTC	TGT	GCA	AGT	GCC	TAC	TAT	GTT	AAC	CAG	GAC	TAC	TGG	GGC	CAA	384
Tyr																
-		95				•	100			•	-	105	-	-		
GGG	ACC	ACT	GTC	ACC	GTC	TCC	TCA	G								409
Gly	Thr	Thr	Val	Thr	Val	Ser	Ser									
	110					115										
SEQ	ID	NO:	8	1												
Sequ	ienc	e L	ena	th:	84	ŀ										
Segu			_			eic	ac:	id								
Stra					ingl											•
Topo					_	-										
robe	TOG	įΥ:	LL	iieg)	<u> </u>											

Molecular Type: Synth tic DNA
Sequ nce
AGCTTGTCAC CGTCTCCTCA GGTGGTGGTG GTTCGGGTGG TGGTGGTTCG GGTGGTGGCG 60
GATCGGACAT CCAGATGACC CAGG
SEQ ID NO: 82
Sequence Length: 84
Sequence Type: Nucleic acid
Strandedness: Single
Topology: Linear
Molecular Type: Synthetic DNA
Sequence
AATTCCTGGG CCATCTGGAT GTCCGATCCG CCACCACCCG AACCACCAC ACCCGAACCA 60
CCACCACCTG AGGAGACGGT GACA 84
SEQ ID NO: 83
Sequence Length: 34
Sequence Type: Nucleic acid
Strandedness: Single
Topology: Linear
Molecular Type: Synthetic DNA
Sequence
CAGCCATGGC GCAGTGTGCA GCTGGTGCAG TCTG 34
SEQ ID NO: 84
Sequence Length: 41
Sequence Type: Nucleic acid
Strandedness: Single
Topology: Linear
Molecular Type: Synthetic DNA
Sequence
CCACCCGAAC CACCACCAC TGAGGAGACG GTGACAGTGG T 41
SEQ ID NO: 85
Sequence Length: 41
Sequence Type: Nucleic acid
Strandedness: Single
Topology: Linear
Molecular Tune: Synthetic DNA

Immediate Source

Sequence
GGGACCACTG TCACCGTCTC CTCAGGTGGT GGTGGTTCGG G 41
SEQ ID NO: 86
S quenc Length: 41
Sequence Type: Nucleic acid
Strandedness: Single
Topology: Linear
Molecular Type: Synthetic DNA
Sequence
GGGCTCTGGG TCATCTGGAT GTCCGATCCG CCACCACCCG A 41
SEQ ID NO: 87
Sequence Length: 44
Sequence Type: Nucleic acid
Strandedness: Single
Topology: Linear
Molecular Type: Synthetic DNA
Sequence
TCGGACATCC AGATGACCCA GAGCCCAAGC AGCCTGAGCG CCAG 44
SEQ ID NO: 88
Sequence Length: 57
Sequence Type: Nucleic acid
Strandedness: Single
Topology: Linear
Molecular Type: Synthetic DNA
Sequence
CAAGAATTCT TATTATTTAT CGTCATCGTC TTTGTAGTCT TTGATTTCGA CCTTGGT 57
SEQ ID NO: 89
Sequence Length: 822
Sequence Type: Nucleic acid
Strandedness: Double
Topology: Linear
Molecular Type: Synthetic
Original Source
Organism: Mouse and human

Clone: pSCFVT7-hM21

Amino acid .1 - 22:leader Amino acid 23 - 139:H chain V r gion Amino acid 140 - 154:Linker Amino acid 155 - 261:L chain V region Amino acid 262 - 269:FLAG Amino acid sequence of Fv polypeptide scFv-hM21 and nucleotide sequence coding therefor Sequence ATG AAA TAC CTA TTG CCT ACG GCA GCC GCT GGA TTG TTA TTA CTC GCT 48 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala 15 GCC CAA CCA GCC ATG GCG CAG GTG CAG CTG GTG CAG TCT GGA GCT GAG 96 Ala Gln Pro Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu 25 20 GTG AAG AAG CCT GGG TCC TCA GTG AAG GTC TCC TGC AAG GCT TCT GGC 144 Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly 35 192 TTC AAC ATT AAA GAC ACC TAT ATA CAC TGG GTG CGC CAG GCT CCA GGA Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly 50 55 60 CAG GGC CTG GAG TGG ATG GGA AGG ATT GAT CCT GCG GAT GGT AAT ACT 240 Gin Gly Leu Glu Trp Met Gly Arg Ile Asp Pro Ala Asp Gly Asn Thr 65 AAA TAT GAC CCG AAG TTC CAG GGC CGA GTC ACA ATC ACT GCA GAC GAA 288 Lys Tyr Asp Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu 90 85 336 TCC ACG AAC ACA GCC TAC ATG GAG CTC AGC CTG AGA TCT GAG GAC Ser Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp 100 105

						1			- 0.	• -					•		
ACA	GCC	TTT	TAT	TTC	TGT	GCA	AGT	GCC	TAC	TAT	GTT	AAC	CAG	GAC	TAC	38	4
	Ala																
		115					120					125					
TGG	GGC	CAA	GGG	ACC	ACT	GTC	ACC	GTC	TCC	TCA	GGT	GGT	GGT	GGT	TCG	. 43	2
Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser		
-	130					135					140						
GGT	GGT	GGT	GGT	TCG	GGT	GGT	GGC	GGA	TCG	GAC	ATC	CAG	ATG	ACC	CAG	48	0
Gly	Gly	Gly	Gly	Ser	G1y	Gly	Gly	Gly	Ser	Asp	Ile	Gln	Met	Thr	Gln		
145					150					155					160		
AGC	CCA	AGC	AGC	CTG	AGC	GCC	AGC	GTG	GGT	GAC	AGA	GTG	ACC	ATC	ACC	52	8
Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	G1y	Asp	Arg	Val	Thr	Ile	Thr	_	
				165					170					175			
TGT	AAG	GCC	AGT	CAG	AAT	GTG	GGT	ACT	AAT	GTA	GCC	TCC	TAC	CAG	CAG	57	6
C <b>y</b> s	Lys	Ala	Ser	Gln	Asn	Val	Gly	Thr	Asn	Va1	Ala	Trp	Tyr	Gln	Gln		
			180					185					190				
	CCA															62	4
Lys	Pro	Gly	Lys	Ala	Pro	Lys	Pro	Leu	11e	Tyr	5er	Ala	Ser	Tyr	Arg.		
		195					200					205					
															GAC	67	2
Tyr	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	GLy	Ser	Gly	Thr	Asp		
	210					215					220						
	ACC															72	0
	Thr	Phe	Thr	Ile		\$er	Leu	Gln	Pro		Asp	Ile	Ala	Thr			
225					230					235					240		
																7.0	
	TGC														ACC	76	•
Tyr	Сув	Gln.	GIn		Asn	261	Tyr	Pro		Ala	Phe	GIÀ	GIn		Inr		
				245					250					255			
						m	4.4.4			C4C	74A	4.4.4				64	. 7
	GTC															80	•
Lys	.Val	GIU		rà a	web	TAX	n y s		vab	vzb	vab	பர்க					
			260					265									
TAA	TA A C	ልልጥ ፣	ኮሮሞሞ	2												82	2
: AA	TAAG	nn:	1011	3												02	-



SEQ ID NO: 90

Sequence Length: 45

S qu nce Type: Nucleic acid

Strand dness: Double

Topology: Linear

Molecular Type: Synthetic

Features: Amino acid sequence of linker region of Fv polypeptide

and nucleotide sequence coding therefor

Sequence

GGT GGT GGT TCG GGT GGT GGT GGT GGT GGC GGA TCG

Gly Gly Gly Ser Gly Gly Gly Gly Gly Gly Gly Ser

10